WEST Search History

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DATE: Friday, April 09, 2004

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ	
☐	L2	L1 same forensic	9
☐	L1	genotype same (mixture or mixed)	848

END OF SEARCH HISTORY

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Search Results - Record(s) 1 through 9 of 9 returned.

☐ 1. Document ID: US 20040067494 A1

L2: Entry 1 of 9   File: PGPB   Apr 8, 2004

PGPUB-DOCUMENT-NUMBER: 20040067494
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20040067494 A1

TITLE: Least-square deconvolution (LSD): a method to resolve DNA mixtures

PUBLICATION-DATE: April 8, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Wang, Tse-Wei	Oak Ridge	TN	US	
Xue, Ning	Knoxville	TN	US	
Birdwell, John D.	Oak Ridge	TN	US	
Rader, Mark	Knoxville	TN	US	
Flaherty, John	Knoxville	TN	US	

US-CL-CURRENT: 435/6; 702/20

ABSTRACT:

Least Square Deconvolution (LSD) uses quantitative allele peak data derived
obtained from a sample containing the DNA of more than one contributor to resolve
the best-fit genotype profile of each contributor. The resolution is based on
finding the least square fit of the mass ratio coefficients at each locus to come
closest to the quantitative allele peak data. Consistent top-ranked mass ratio
combinations from each locus can be pooled to form at least one composite DNA
profile at a subset of the available loci. The top-ranked DNA profiles can be used
to check against the profile of a suspect or be used to search for a matching
profile in a DNA database.

L2: Entry 1 of 9   File: PGPB   Apr 8, 2004

DOCUMENT-IDENTIFIER: US 20040067494 A1
TITLE: Least-square deconvolution (LSD): a method to resolve DNA mixtures

Summary of Invention Paragraph:
[0007] Until now, the deconvolution of mixed DNA profiles contributed by multiple
people has been one of the most challenging tasks facing forensic scientists. Part
of the difficulty derives from the large number of possible genotype combinations

that can be exhibited by the multiple contributors (4) in the mixed DNA profile. So far, no analytical and reliable method has been published for the resolution of DNA mixture into its components.

Summary of Invention Paragraph:
[0009] More recently, in 1998, the British group of P. Gill et al. of the Forensic Science Services (5) presented a novel method to resolve DNA mixtures using quantitative allele peak data. This method requires an iterative search for the optimum mass ratio to fit the allele peaks at each locus that an individual can contribute to a sample. For each mass ratio used to fit each possible genotype profile, the residuals between the expected allele peak areas and those obtained from the measured allele peaks are calculated. The smallest residual at each locus is added to the minimum residuals similarly derived from allele peak data available at other loci. The genotype combinations that give the overall lowest minimum residual are selected to be the best-fit genotype combinations for the loci. This method is limiting and artificial because a finite set of prior-determined mass ratios is used to calculate the fitting residual. Further, this method is labor intensive because iterations are involved in searching for the best-fit genotype combinations.

Detail Description Paragraph:
Application of Least Square Approach (LSD) Principles Resolves a Mixed Forensic DNA Sample into Each Contributor's Genotype

Detail Description Paragraph:
[0204] To further test the functionality and effectiveness of the LSD method, five additional sets of allele peak data from forensic mixed DNA samples were run using LSD. The DNA mixture data were obtained from swabs in rape cases. The genotype of the female victim is known in each case. Sperm fraction in the mixture sample was separated from the mixture evidence by differential extraction. Therefore, genotype profiles of the male perpetrators are also obtained for all five samples. LSD was applied to the mixture data and the LSD suggested results were compared to the known genotype profiles of the two contributors. Among the five sets of data, four have peak area information at nine loci, and the fifth has information at twelve loci. Two of the five sets of DNA mixture data from Corpus Christi and the corresponding LSD suggested genotype resolution results are discussed in Examples 8A-B.

| Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw De |

☐ 2.   Document ID: US 20030219815 A1

L2: Entry 2 of 9   File: PGPB   Nov 27, 2003

PGPUB-DOCUMENT-NUMBER: 20030219815
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20030219815 A1

TITLE: Methods and apparatus for genotyping

PUBLICATION-DATE: November 27, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Gill, Peter	Birmingham		GB	

Dixon, Lindsey   Birmingham   GB

US-CL-CURRENT: 435/6; 702/20

ABSTRACT:

A method for establishing the genotype of the locus is provided in which a series
of calibration samples are analysed, the results being one of three indication
types, a window being defined relative to the indication for each of the indication
types, unknown samples being similarly analysed with the window that they fall
within being taken to determine the indication type for the unknown sample and
hence the genotype of the relevant locus.

The technique provides a robust, reliable and accurate method of genotyping which
is suited to automation.
    L2: Entry 2 of 9   File: PGPB   Nov 27, 2003

DOCUMENT-IDENTIFIER: US 20030219815 A1
TITLE: Methods and apparatus for genotyping

Detail Description Paragraph:
[0050] To be truly reliable for forensic applications, include use as evidence in a
court of law, the genotype considered as being indicated by the analysis must be
robust. The yes/no type answer used in medical diagnosis has been established by
the applicant to be insufficient. Hence the applicant has developed a quantitative
analysis towards this aim. To extend this quantitative analysis further and make it
suitable for automation and ideally incorporation into an expert system whilst
achieving sufficient standards in reliability and consistency of interpretation the
applicant has developed the techniques of the present invention. In developing
these techniques it is also necessary to bear in mind that compared with medical
applications, where the sample to be tested is collected direct from the person of
interest under controlled conditions, the samples in forensic contexts may be less
than perfect for a variety of reasons. For instance, the sample collected may be
small and/or aged and/or a mixture of DNA from more than one source and are
indirectly collected. Any expert system must therefore be able to cope with all of
these issues at yet be reliable and robust.

| Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw De |

3. Document ID: US 20030082576 A1
    L2: Entry 3 of 9   File: PGPB   May 1, 2003

PGPUB-DOCUMENT-NUMBER: 20030082576
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20030082576 A1

TITLE: High throughput polymorphism screening

PUBLICATION-DATE: May 1, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Jones, Keith	Sunnyvale	CA	US	
Leuther, Kerstin	Palo Alto	CA	US	
Shapero, Michael H.	Redwood City	CA	US	

US-CL-CURRENT: 435/6; 435/91.2

ABSTRACT:

Methods are provided for determining the identity of a polymorphic nucleotide in a
complex mixture of nucleic acids where one or more distinct polymorphisms can be
present in the mixture, and multiple polymorphisms can be screened in parallel.
Target nucleic acids are amplified using bridge amplification techniques. The
detection and identification of the specific polymorphic residue(s) is based on
readout methods that utilize the specificity of specific enzymes for complementary
DNA sequences. These approaches result in a labeled nucleotide covalently attached
to the amplicon, where the identity of the nucleotide is informative of the
polymorphic sequence. In one aspect, the readout process uses primer extension
protocols, where the specific base incorporated by DNA polymerase is determined by
the sequence at the polymorphic site. In another aspect, the identity of a specific
base hybridized and ligated to the amplicon is determined by the sequence at the
polymorphic site. The polynucleotide to which the label has been attached can be
detected in situ, i.e. bound to the solid substrate used for amplification; or can
be released and detected.
    L2: Entry 3 of 9   File: PGPB   May 1, 2003

DOCUMENT-IDENTIFIER: US 20030082576 A1
TITLE: High throughput polymorphism screening

Detail Description Paragraph:
[0023] Many polymorphisms have been identified and some have been linked to known
diseases. For example, sickle cell anemia, cystic fibrosis, and diabetes have all
been linked to genomic polymorphisms. However, many polymorphisms have yet to be
analyzed for association with disease. Knowledge of genetic variation in an
individual is important not only for diagnosis of genetic predisposition to many
diseases, but also for genetically controlled differences in metabolism and
response to therapeutic agents. Variation can also be used to determine which genes
contribute to multigenic or quantitative traits such as increased susceptibility to
diseases or for understanding why some strains of a microbe are exceptionally
virulent. For example, linkage analysis of polymorphism genotypes in a diseased and
control population can be used to narrow down the area of search on a chromosome
for a disease-associated gene (Riley, et al. (2000) Pharmacogenetics 1:39-47).
Furthermore, genetic variation can be employed for diagnostics, identification
purposes, both in microbiology and in forensics, for studies of recombination, and
in population genetics. The methods of the present invention allow simultaneous and
efficient screening of a complex mixture of nucleic acids for many known
polymorphisms in a single reaction chamber. Also provided are kits for use in
screening a nucleic acid sample for known polymorphisms.

| Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw D |

☐ 4.   Document ID: US 20020152035 A1

L2: Entry 4 of 9   File: PGPB   Oct 17, 2002

PGPUB-DOCUMENT-NUMBER: 20020152035
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020152035 A1

TITLE: Method and system for DNA mixture analysis

PUBLICATION-DATE: October 17, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Perlin, Mark W.	Pittsburgh	PA	US	

US-CL-CURRENT: 702/20

ABSTRACT:

The present invention pertains to a process for automatically analyzing mixed DNA
samples. Specifically, the process comprises the steps of obtaining a mixed DNA
sample; amplifying the DNA sample to produce a product; detecting the product to
produce a signal; and analyzing the signal to determine information about the
composition of the mixed DNA sample. This DNA mixture analysis is useful for
finding criminals and convicting them. This mixture analysis provides high quality
estimates, and can determine genotypes, mixture weights, and likelihood ratios.
This analysis provides confidence measures in the results it computes, and
generates reports and intuitive visualizations. The process automates a tedious
manual procedure, thereby reducing the cost, time, and effort involved in DNA
forensic analysis. The system can greatly accelerate the rate of DNA crime
analysis, and be used to exonerate innocent people.
    L2: Entry 4 of 9   File: PGPB   Oct 17, 2002

DOCUMENT-IDENTIFIER: US 20020152035 A1
TITLE: Method and system for DNA mixture analysis

Abstract Paragraph:
The present invention pertains to a process for automatically analyzing mixed DNA
samples. Specifically, the process comprises the steps of obtaining a mixed DNA
sample; amplifying the DNA sample to produce a product; detecting the product to
produce a signal; and analyzing the signal to determine information about the
composition of the mixed DNA sample. This DNA mixture analysis is useful for
finding criminals and convicting them. This mixture analysis provides high quality
estimates, and can determine genotypes, mixture weights, and likelihood ratios.
This analysis provides confidence measures in the results it computes, and
generates reports and intuitive visualizations. The process automates a tedious
manual procedure, thereby reducing the cost, time, and effort involved in DNA
forensic analysis. The system can greatly accelerate the rate of DNA crime
analysis, and be used to exonerate innocent people.

Detail Description Paragraph:
[0080] Others have computed mixture weights by minimizing parameters at single loci
(Gill P, Sparkes R, Pinchin R, Clayton T M, Whitaker J P, Buckleton J. Interpreting
simple STR mixtures using allele peak area. Forensic Sci. Int. 1998;91:41-53). In
the LMA model, this early work can be reinterpreted as minimizing at a single locus

the sum of squares deviation .parallel.d-G.multidot.w.parallel..sup.2 over w for each feasible integer-valued genotype matrix G. This prior art has a limited single-locus view of the data, which restricts the amount of derivable useful information; there is no known way to combine the separate single locus partial solutions into one global optimum. Moreover, such prior art does not make special use of the known reference genotypes, which contain much valuable information. LMA improves on such earlier mixture methods by providing a mathematical basis that can use the data from all the loci simultaneously in a rapid optimized numerically computed global minimization. Moreover, LMA permits the genotype matrix entries to assume any possible value, and not just integers.

Detail Description Paragraph:
[0100] Consider next the case where the mixture weights w are not known, with J=2, genotype a is known, but genotype b is not known. The goal is to make inferences about the genotype matrix G starting from a mixture data profile d. This case has practical applications for forensic science. In one typical scenario, a stain from a crime scene may contain a DNA mixture from the victim and an unknown individual, the victim's DNA is available, and the investigator would like to connect the unknown individual's DNA profile with a candidate perpetrator. This scenario typically occurs in rape cases. The perpetrator may be a specific suspect, or the investigator may wish to check the unknown individual's DNA profile against a DNA database of possible candidates. If the mixture weight wA were known, then the genotype b could be computed immediately from the vector difference operation (with known weights) just described.

Detail Description Paragraph:
[0113] Minimize this function over w in [0,1] to find wA, and estimate b from the computed b(wA). If desired, the summation terms can be normalized to reflect alternative weightings of the loci or alleles, e.g., based on variance. Other heuristic functions can be used that reflect reasonable constraints on the genotype vectors (Gill P, Sparkes R, Pinchin R, Clayton T M, Whitaker J P, Buckleton J. Interpreting simple STR mixtures using allele peak area. Forensic Sci. Int. 1998;91:41-53), incorporated by reference.

Detail Description Paragraph:
[0114] To assess the quality of the computed STR profile, use information from this minimization search. Rule checking can identify potentially anomalous allele calls, particularly when peak quantities or sizes do not conform to expectations (Perlin M. Computer automation of STR scoring for forensic databases. In: First International Conference on Forensic Human Identification in The Millennium; 1999; London, UK: The Forensic Science Service; 1999), incorporated by reference. Quality measures can be computed on the genotypes, which may suggest problematic calls even when no rule has fired. A most useful quality score in this mixture analysis is the deviation dev(e) of the computed genotype. Low deviations indicate a good result, whereas high scores suggest a poor result. It may be helpful to partition the deviations by locus, using the locus deviation function dev.sub.locus(e). When a locus has an unusually high deviation, it can be removed from the profile, and the resulting partial profile then used for human identity matching.

Detail Description Paragraph:
[0221] by appropriately weighting the prior probabilities Pr{b.sub.i} based on the weight of evidence in the data Pr{d.vertline.a,b.sub.i} represents a strikingly useful advance over the prior art. Current forensic reporting practice typically uses full weighting of all possible genotypes in a mixture (National Research Council, Evaluation of Forensic DNA Evidence: Update on Evaluating DNA Evidence, 1996, Washington, DC: National Academy Press), incorporated by reference. At each locus, then, the full weight of each possible genotype is currently used, instead of the weight as determined by the data. Examining the effect on the denominator is shown by: 20 genotype i P r { d | a , b i } P r { b i } (1) P r { b 1 } (2) genotype i P r { b i }

Detail Description Paragraph:
[0319] (Other lab data) The automation methods were applied to data from other laboratories, obtaining accurate results. For example, there was a reanalysis of the original six locus STR data (provided by Dr. Peter Gill) underlying the quantitative analysis of mixture sample MT/NO in (Gill P, Sparkes R, Pinchin R, Clayton T M, Whitaker J P, Buckleton J. Interpreting simple STR mixtures using allele peak area. Forensic Sci. Int. 1998;91:41-53), incorporated by reference. Taking individual MT as the known reference profile, for each approximate mixing ratio (1:10, 1:5, 1:2, 1:1, 2:1, 5:1, 10:1), exact mixture weights were derived and individual NO's genotype was estimated. The respective computed weights (10.02%, 13.83%, 27.87%, 41.89%, 58.43%, 77.25%, 86.66%) are in close agreement with the four allele locus weights that they had estimated (Table 6 for 5 ng DNA in Gill P, Sparkes R, Pinchin R, Clayton T M, Whitaker J P, Buckleton J. Interpreting simple STR mixtures using allele peak area. Forensic Sci. Int. 1998;91:41-53).

Detail Description Paragraph:
[0324] Unique identification of individual components of mixed DNA samples is useful for finding suspects from DNA evidence, and for identifying individuals from DNA data in forensic and nonforensic situations. An individual's genotype can be matched against a database for definitive identification. This database might include evidence, victims, suspects, other individuals in relevant cases, law enforcement personnel, or other individuals (e.g., known offenders) who might be possible candidates for matching the genotype. In one preferred embodiment, the database is a state, national or international DNA database of convicted offenders.

Detail Description Paragraph:
[0335] As discussed, with the random person hypothesis of the defense, current LR analysis gives far too much away to the defense (National Research Council, Evaluation of Forensic DNA Evidence: Update on Evaluating DNA Evidence, 1996, Washington, DC: National Academy Press), incorporated by reference. Linear mixture analysis can reduce such inflated LRs by many orders of magnitude. The LR can be improved by using standard bootstrapping techniques on the population frequencies to remove much of the sampling error. It is preferable to consider inbreeding coefficients when computing the prior genotype probabilities from the allele frequencies.

Detail Description Paragraph:
[0345] To prevent this database corruption with mixed DNA profiles, it would be useful to clean up the entries prior to their inclusion on the database. When the raw (or other quantitative) STR data are available, this clean up is readily implemented by the mixture deconvolution invention. For example, consider the common case of a two person mixture containing a known victim and an unknown perpetrator. Mixture deconvolution estimates the genotype of the unknown perpetrator, along with a confidence. (Lower confidences may suggest intelligently using degenerate alleles at some loci.) The resolved unknown perpetrator genotypes are then entered into the forensic database, rather than the usual qualitative (e.g., major and minor peak) multiplicity of degenerate alleles. The result is far more uniqueness in subsequent DNA query matches, with an associated increase in the informativeness and utility of the matches.

| Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw D |

☐ 5.   Document ID: US 6670124 B1

L2: Entry 5 of 9   File: USPT   Dec 30, 2003

US-PAT-NO: 6670124
DOCUMENT-IDENTIFIER: US 6670124 B1

TITLE: High throughput methods of HLA typing

DATE-ISSUED: December 30, 2003

INVENTOR-INFORMATION:
NAME	CITY	STATE	ZIP CODE	COUNTRY
Chow; Robert	Arcadia	CA		
Tonai; Richard	Valencia	CA		

US-CL-CURRENT: 435/6; 435/91.2, 536/23.1, 536/24.3, 536/24.31

ABSTRACT:

A method for determining an HLA genotype of a subject is disclosed. The method
comprises (a) isolating template nucleic acid from the subject; (b) amplifying the
template nucleic acid to generate sufficient product for each allele of at least
one gene locus to be determined; (c) hybridizing the template nucleic acid with an
immobilized array of capture oligonucleotides, each having a known nucleic acid
sequence of an HLA allele; and (d) determining the particular capture
oligonucleotide to which the template nucleic acid hybridizes, thereby determining
the genotype of the subject. A number of additional methods that can eliminate or
abbreviate additional steps are also described. Moreover, the present invention
provides a method for determining tissue compatibility using the determined HLA
genotype.

8 Claims, 0 Drawing figures
Exemplary Claim Number: 1
   L2: Entry 5 of 9   File: USPT   Dec 30, 2003

DOCUMENT-IDENTIFIER: US 6670124 B1
TITLE: High throughput methods of HLA typing

Other Reference Publication (1):
Allele-Specific HLA-DRB1 Amplificationof Forensic Evidence Samples with Mixed
Genotypes--Marie Allen, Tom Saldeen and Ulf Gyllensten--1995.*

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw De |

☐ 6. Document ID: US 6440707 B1
   L2: Entry 6 of 9   File: USPT   Aug 27, 2002

US-PAT-NO: 6440707
DOCUMENT-IDENTIFIER: US 6440707 B1

TITLE: Fluorescence polarization in nucleic acid analysis

DATE-ISSUED: August 27, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Kwok; Pui-Yan	St. Louis	MO		
Chen; Xiangning	St. Louis	MO		
Levine; Leanna	Redondo Beach	CA		

US-CL-CURRENT: 435/91.2; 435/6, 435/91.1, 435/91.41, 536/22.1, 536/23.1, 536/24.3, 536/24.31, 536/24.32, 536/24.33

ABSTRACT:

A new method for DNA diagnostics based on template-directed primer extension and detection by fluorescence polarization is described. In this method, amplified genomic DNA fragments containing polymorphic sites are incubated with a oligonucleotide primer designed to hybridize to the DNA template adjacent to the polymorphic site in the presence of allelic dye-labeled dideoxyribonucleoside triphosphates and a modified Taq DNA polymerase. The primer is extended by the dye-terminator specific for the allele present on the template. At the end of the reaction, the fluorescence polarization of the two dye-terminators in the reaction mixture are analyzed directly without separation or purification. This homogeneous DNA diagnostic method is shown to be highly sensitive and specific and is suitable for automated genotyping of large number or samples.

12 Claims, 2 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 2
    L2: Entry 6 of 9   File: USPT   Aug 27, 2002

DOCUMENT-IDENTIFIER: US 6440707 B1
TITLE: Fluorescence polarization in nucleic acid analysis

Detailed Description Text (68):
These studies demonstrate that the FP-TDI assay is a robust, homogeneous genetic test that requires no modified primers for its execution while retains the sensitivity and specificity of the primer extension reaction. Since the unmodified FP-TDI primer cost is only 20% of that of a dye-labeled primer, this new detection method is more cost effective than other genotyping assays based on dye-labeled probes. Demand for DNA testing (i.e., assaying for the presence or absence of known DNA polymorphisms or mutations) is expected to increase dramatically in the areas of diagnostics, forensics, and population studies. A homogeneous genotyping assay such as the FP-TDI assay is highly suitable for large scale genetic studies because it is not limited by a particular reaction format and it offers the flexibility of using the best markers as they become available for a particular application without redesigning or re-fabricating high-density DNA chips. Furthermore, the FP-TDI assay is simple to set up (by adding the standard reagent mixture to the DNA template), the results are obtained in electronic form minutes after the allele-discriminating reaction is performed, and the genotype can be assigned automatically by the use of a simple computer program. Since the principle of FP applies to any fluorescent dye, including those absorbing in the infrared region, studies are now underway to identify a set of 4 optimal fluorescent dyes to produce a standard set of reaction conditions suitable for multiplex TDI. As DNA diagnostic tests will no doubt be performed more and more by clinical rather than research laboratories, methods (such as the FP-TDI assay) utilizing standard protocols that require minimal laboratory skills or manual handling will be crucial to the clinical practice of medicine in the future.

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | | Claims | KWIC | Draw De |

☐ 7.   Document ID: US 6180408 B1

L2: Entry 7 of 9   File: USPT   Jan 30, 2001

US-PAT-NO: 6180408
DOCUMENT-IDENTIFIER: US 6180408 B1

TITLE: Fluorescence polarization in nucleic acid analysis

DATE-ISSUED: January 30, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Kwok; Pui-Yan	St. Louis	MO		
Chen; Xiangning	St. Louis	MO		
Levine; Leanna	Redondo Beach	CA		

US-CL-CURRENT: 436/6; 435/91.1, 435/91.2, 435/91.41, 536/22.1, 536/23.1, 536/24.3, 536/24.31, 536/24.32, 536/24.33

ABSTRACT:

A new method for DNA diagnostics based on template-directed primer extension and detection by fluorescence polarization is described. In this method, amplified genomic DNA fragments containing polymorphic sites are incubated with a oligonucleotide primer designed to hybridize to the DNA template adjacent to the polymorphic site in the presence of allelic dye-labeled dideoxyribonucleoside triphosphates and a modified Taq DNA polymerase. The primer is extended by the dye-terminator specific for the allele present on the template. At the end of the reaction, the fluorescence polarization of the two dye-terminators in the reaction mixture are analyzed directly without separation or purification. This homogeneous DNA diagnostic method is shown to be highly sensitive and specific and is suitable for automated genotyping of large number or samples.

13 Claims, 2 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 2
    L2: Entry 7 of 9   File: USPT   Jan 30, 2001

DOCUMENT-IDENTIFIER: US 6180408 B1
TITLE: Fluorescence polarization in nucleic acid analysis

Detailed Description Text (68):
These studies demonstrate that the FP-TDI assay is a robust, homogeneous genetic test that requires no modified primers for its execution while retains the sensitivity and specificity of the primer extension reaction. Since the unmodified FP-TDI primer cost is only 20% of that of a dye-labeled primer, this new detection method is more cost effective than other genotyping assays based on dye-labeled

probes. Demand for DNA testing (i.e., assaying for the presence or absence of known
DNA polymorphisms or mutations) is expected to increase dramatically in the areas
of diagnostics, forensics, and population studies. A homogeneous genotyping assay
such as the FP-TDI assay is highly suitable for large scale genetic studies because
it is not limited by a particular reaction format and it offers the flexibility of
using the best markers as they become available for a particular application
without redesigning or re-fabricating high-density DNA chips. Furthermore, the FP-
TDI assay is simple to set up (by adding the standard reagent mixture to the DNA
template), the results are obtained in electronic form minutes after the allele-
discriminating reaction is performed, and the genotype can be assigned
automatically by the use of a simple computer program. Since the principle of FP
applies to any fluorescent dye, including those absorbing in the infrared region,
studies are now underway to identify a set of 4 optimal fluorescent dyes to produce
a standard set of reaction conditions suitable for multiplex TDI. As DNA diagnostic
tests will no doubt be performed more and more by clinical rather than research
laboratories, methods (such as the FP-TDI assay) utilizing standard protocols that
require minimal laboratory skills or manual handling will be crucial to the
clinical practice of medicine in the future.

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw. D |

☐   8.   Document ID: US 5521301 A

L2: Entry 8 of 9   File: USPT   May 28, 1996

US-PAT-NO: 5521301
DOCUMENT-IDENTIFIER: US 5521301 A

TITLE: Genotyping of multiple allele systems

DATE-ISSUED: May 28, 1996

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Wallace; R. Bruce	Pasadena	CA		
Ugozzoli; Luis	Arcadia	CA		

US-CL-CURRENT: 536/24.33; 435/6, 435/91.2

ABSTRACT:

Disclosed is an application of allele specific polymerase chain reaction technology
for the direct determination of multiple allele genotyping. ABO genotyping is
demonstrated with allele specific primer sets.

2 Claims, 4 Drawing figures
Exemplary Claim Number: 2
Number of Drawing Sheets: 4

L2: Entry 8 of 9   File: USPT   May 28, 1996

DOCUMENT-IDENTIFIER: US 5521301 A
TITLE: Genotyping of multiple allele systems

Brief Summary Text (7):
This invention provides a novel application of the ASPCR technique used to genotype
multiple allele systems. In particular, the invention is useful to determine the
ABO genotypes of individuals without the need of family analysis. The method
introduces a new strategy for primer design which permits the identification of the
different ABO genotypes according to the molecular size of allele specific
amplification products. Four primer sets each specific for a different set of ABO
alleles are mixed in one reaction and the amplification products resolved on a
polyacrylamide gel. Forty one individuals belonging to various families, whose ABO
genotype were previously determined serologically, were typed with this new
variation of the ASPCR technique. A 100% correlation was found between the serology
and ASPCR data. The Mendelian segregation of ABO alleles was also demonstrated in
families. The method is rapid, simple, reproducible, and specific. The
determination of ABO genotypes is one example of the invention which is useful
broadly to determine the genotypes of multiple systems such as HLA and in gene
mapping, genetic disease diagnosis, paternity testing and forensic science
techniques.

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw D |

☐ 9. Document ID: EP 1229135 A2

L2: Entry 9 of 9   File: EPAB   Aug 7, 2002

PUB-NO: EP001229135A2
DOCUMENT-IDENTIFIER: EP 1229135 A2
TITLE: Method and system for DNA mixture analysis

PUBN-DATE: August 7, 2002

INVENTOR-INFORMATION:
NAME   COUNTRY
PERLIN, MARK W   US

INT-CL (IPC): C12 Q 1/68; G06 F 19/00; G06 F 17/00

ABSTRACT:

CHG DATE=20020903 STATUS=O> The present invention pertains to a process for
automatically analyzing mixed DNA samples. Specifically, the process comprises the
steps of obtaining a mixed DNA sample; amplifying the DNA sample to produce a
product; detecting the product to produce a signal; and analyzing the signal to
determine information about the composition of the mixed DNA sample. This DNA
mixture analysis is useful for finding criminals and convicting them. This mixture
analysis provides high quality estimates, and can determine genotypes, mixture
weights, and likelihood ratios. This analysis provides confidence measures in the
results it computes, and generates reports and intuitive visualizations. The
process automates a tedious manual procedure, thereby reducing the cost, time, and
effort involved in DNA forensic analysis. The system can greatly accelerate the

rate of DNA crime analysis, and be used to exonerate innocent people.

L2: Entry 9 of 9   File: EPAB   Aug 7, 2002

DOCUMENT-IDENTIFIER: EP 1229135 A2
TITLE: Method and system for DNA mixture analysis

Abstract Text (1):
CHG DATE=20020903 STATUS=O> The present invention pertains to a process for
automatically analyzing mixed DNA samples. Specifically, the process comprises the
steps of obtaining a mixed DNA sample; amplifying the DNA sample to produce a
product; detecting the product to produce a signal; and analyzing the signal to
determine information about the composition of the mixed DNA sample. This DNA
mixture analysis is useful for finding criminals and convicting them. This mixture
analysis provides high quality estimates, and can determine genotypes, mixture
weights, and likelihood ratios. This analysis provides confidence measures in the
results it computes, and generates reports and intuitive visualizations. The
process automates a tedious manual procedure, thereby reducing the cost, time, and
effort involved in DNA forensic analysis. The system can greatly accelerate the

rate of DNA crime analysis, and be used to exonerate innocent people.

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw D |

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Term	Documents
FORENSIC	6743
FORENSICS	1585
(1 SAME FORENSIC).PGPB,USPT,EPAB,JPAB,DWPI.	9
(L1 SAME FORENSIC).PGPB,USPT,EPAB,JPAB,DWPI.	9

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